

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2002, 05:44:19 ; Search time 43.44 Seconds
(without alignments)
922.506 Million cell updates/sec

Title: US-09-652-292-2

Perfect score: 2765

Sequence: 1 MGHSPVLPICASVLLGGL.....CHRONSTGIPYSRIEISAAS 541

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	568	20.5	526	20 AAY02168	A facilitative glu
2	556	20.1	629	22 AAB66935	Human GLUTX2. Hom
3	556	20.1	629	22 AAB66940	GLUTX2 consensus s
4	543	19.6	618	22 AAB66936	Rat GLUTX2. Rattu
5	541	19.6	582	21 AAG29528	Arabidopsis thalia
6	536.5	19.4	555	21 AAG29529	Arabidopsis thalia
7	517.5	18.7	480	22 AAM00107	Sugar transporter
8	507	18.3	551	20 AAY50799	Spinach glucose tr
9	506	18.3	478	21 AAG15416	Arabidopsis thalia
10	506	18.3	493	21 AAG15415	Arabidopsis thalia
11	506	18.3	546	21 AAG15414	Arabidopsis thalia

12	504	18.2	491	21 AAB12594	Brevibacterium lac
13	502	18.2	491	22 AAG89949	C glutamicum prote
14	500.5	18.1	518	20 AAY49632	Soybean hexose car
15	488.5	17.7	522	21 AAG52315	Arabidopsis thalia
16	482.5	17.5	522	21 AAG16798	Arabidopsis thalia
17	479	17.3	491	21 AAG52316	Arabidopsis thalia
18	478	17.3	477	22 AAE04888	Human transporter
19	475	17.2	508	21 AAG29530	Arabidopsis thalia
20	474.5	17.2	478	22 AAB66933	GLUTX3 consensus s
21	473	17.1	491	21 AAG16799	Arabidopsis thalia
22	470	17.0	477	22 AAB66932	Human GLUTX1. Hom
23	466.5	16.9	491	21 AAG32072	Arabidopsis thalia
24	466.5	16.9	508	21 AAG32071	Arabidopsis thalia
25	465.5	16.8	478	22 AAB66939	GLUTX1 consensus s
26	460.5	16.7	507	22 AAB66941	GLUTX3 consensus s
27	460	16.6	473	21 AAG52317	Arabidopsis thalia
28	457.5	16.5	474	19 AAW58862	T. halophilus xyul
29	455	16.5	507	22 AAB66937	Human GLUTX3. Hom
30	454	16.4	473	21 AAG16800	Arabidopsis thalia
31	450	16.3	477	22 AAB66934	Murine GLUTX1. Mu
32	438.5	15.9	511	20 AAY49630	Rice hexose carrie
33	437	15.8	492	21 AAB13225	H17B01.1-GFP fusio
34	433.5	15.7	474	21 AAG50066	Arabidopsis thalia
35	429.5	15.5	466	21 AAG32073	Arabidopsis thalia
36	427	15.4	493	20 AAY27292	Glucose transporte
37	427	15.4	493	22 AAB30522	Amino acid sequenc
38	418.5	15.1	522	18 AAW17836	Rat glucose transp
39	417	15.1	517	20 AAY49633	Wheat hexose carri
40	414	15.0	508	22 AAG93128	C glutamicum prote
41	407.5	14.7	503	22 AAB66938	Rat GLUTX3. Rattu
42	407.5	14.7	509	20 AAY27290	Glucose transporte
43	404.5	14.6	494	20 AAY27289	Glucose transporte
44	397.5	14.4	415	21 AAG50067	Arabidopsis thalia
45	396.5	14.3	502	20 AAY49625	Corn hexose carrie

ALIGNMENTS

RESULT 1
AAY02168
ID AAY02168 standard; Protein; 526 AA.
XX
AC AAY02168;
XX
DT 08-JUL-1999 (first entry)
XX
DE A facilitative glucose transporter protein GLUT8.
XX
KW Facilitative glucose transporter protein; GLUT8; malignancy;
KW breast cancer; prostate cancer; epithelial cell cancer;
KW non-insulin-dependent diabetes mellitus; insulin resistance;
KW central obesity; hypertension; dyslipidaemia; glucose intolerance;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO9918125-A1.
XX
PD 15-APR-1999.
XX
PF 30-SEP-1998; 98WO-AU00819.
XX
PR 01-OCT-1997; 97AU-0009573.
XX
PA (SVIN-) ST VINCENT'S INST MEDICAL RES.
XX
PI Best JD, Rogers SB;
XX
DR WPI: 1999-277253/23.
XX
DR N-PSDB; AAX35516.
XX
PT Nucleic acid encoding a facilitative glucose transporter

[illegible]

QY 267 SSAVLASVGLCAVKAAATLTMGLVDGRALL-----LAGCALMALSVSGIGLYSFA 320
 Db 313 ktamalslitsginalgsivmmfvdrygrkmlismfgliaclliatcvfsqaal-ha 371
 QY 321 VPMDSGPSCLAVPNATGOTGLPGDGLLOPSSLPPIPTNEDOREPILSTAKKTKPHPRS 380
 Db 372 kldafesrtfapnatesayap-----laenapp-----srwcmkclrsecgfcas 419
 QY 381 G-DPSAPRLALSSALPGPLPARGHALLR-----WTALLCLMVFAFSGFGPVT 431
 Db 420 gvqpyagacvvsddmkatccsgrtffkdgcpskfgflaiflgyivvyapgmgtvp 479
 QY 432 WLVLSEIYVEIRGAPAFACNSFNAAALFISLSFLDLICTIGLSTWTFLLYGLTAVLGLG 491
 Db 480 winseilyplyrglvgglaavsnvsnlivsesflsthalssgtflifagfstiglf 539
 QY 492 FIVLFVPETKQSLAEIDQ 510
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RESULT 6

AAG29529 ID AAG29529 standard; Protein: 555 AA.

AC AAG29529;
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 XX
 DT 17-OCT-2000 (first entry)
 XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX
 XX
 PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
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Oy 4 SPVPLPCASVSLGCLTGFYELAVISGALLPLODFGL--SCLQEFLVGLSLLGALLA 61
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Db 107 sasvlpy-vgvaclgallfghlvgvngaldylsadlalatgnvtlqgwwvslilagatvg 165
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 62 SILVGFLLDCYGRKQAILGSLNVLGASLTGLAGSLAWLVGRAVVGFAISLSMACCI 121
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Oy 122 YVSELVGRQRCGLVSLYEAGTIVGILLSYALNVALAGTGWGRHMFGMATAPVLOSL 181
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Db 226 yiselptelgaigsvnqlfciigilaalvaglplagnplwrlumfglatvpvllalg 285
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Oy 182 LLFLPAGT-----DEPATHKDLIPLQGE-----APKLGPCRPRYSFLDLERA 224
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Oy 225 RDNRGRTTVGLVLFQOLTGPQNVLCYASTIFSSVGFHGSSAVLASVGLGAVKYAAT 284
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Oy 285 LTAMGLVDRAGRALLAGCALMALSVSGIGLVSPVPMDSCLAVPNATGQTGLPCD 344
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Oy 405 HALLRWTALLCLMWVSAFSGFGPVTWLVSEIYPVEIRGRAFAFCNSFWAAMLFISL 464
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Oy 465 SFLOLIGTIGLSWTELLYGLTAVLIGLGFYILFVPETKGSIAEID 509
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RESULT 9
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ID AAG15416 standard; Protein; 478 AA.
XX
AC AAG15416;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15660.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 15659.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD 06-SEP-2000.
PF
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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Query Match      18.3%; Score 506; DB 21; Length 493;
Best Local Similarity 29.5%; Pred. No. 1.6e-37;
Matches 155; Conservative 68; Mismatches 196; Indels 106; Gaps 8;

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Db 49 egtvlpf-vgvacigallfghlgvngaleylakldiaentvlgqgwivslagacvg 107
QY 62 SLVGFLLDCVGRKQAILGSLNVLGASLUTLGLAGSLAWLVGRAVVGFAISLSMACCI 121
Db 108 sftggaladkfgtrttfqlaipaigaflcatqsgvqtmivgrllagigigissaiypl 167
QY 122 YVSELVGRQRQVLSVLEAGTGVGILLSYALNVALACTPGWRHMFQGNATAPAVLQSL 181
Db 168 ylselspteifgalsvsnqlfctigilaallagiplaanplwrtumfgvavipsvllaig 227
QY 182 LLFLPAGT-----DETATHKDLIPQGG-----APKLGPGRPRYSFLDLFRA 224
Db 228 mafspesprfwlvggkvseaeakltlygkervvelvrdlsasgggssepeagwfdlfs 287
QY 225 RDNMRGRTTVGLGLVLFQOLTGQPNVLCYASTIFSSVGFHGGSSAVLASVGLGAVKVAAT 284
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QY 285 LTAMGLVDRAGRALLAGCALMALSVSGTGLYFAVPMDSGSPCLAVPNATGCTGLPGD 344
Db 343 avasslmdkmgrksllltsfgmalism----- 369
QY 345 SGLLODSSLPIPTNEDQREPILSTAKKTKPHRSGDPSAPPRLALSSALPGPLPARG 404
Db 370 -----lllsisftwkaalaays 395
QY 405 HALLRTALLCLMVFYSAFSGFGPVTWLVLSIYVEINGRAFAFCNSFNWAAFLISL 464
Db 386 gtl----avgtvlyvlslfsgagpyalllpeifasrirakavalslgmhwisnfvigl 441
QY 465 SFLLDITIGLSWTFLYGLTAVLGLGFIYLFVPETKGQSLAID 509
Db 442 yflsvvckfgisvvygfagvcvlayviagnvvctgrsleie 486

RESULT 11
AAG15414
ID AAG15414 standard; Protein; 546 AA.
XX
AC AAG15414;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15658.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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Query Match 18.3%; Score 506; DB 21; Length 546;
 Best Local Similarity 29.5%; Pred. No. 1.8e-37;
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 QY 62 SLVGGFLIDCYGRKQAILGSNLVLLAGSLTGLAGSLAMVLVGRVAVGFAISLSSMACCI 121
 DB 161 sftggaladkgrtrfqiadaipalgaflcatagvqtmivgrllagigigissalvpl 220
 QY 122 YVSELVGPQRGVLSVLYEAGITVIGLLSYALNYALAGTIPWGRHMFGRWATAPAVLOSLS 181
 DB 221 yiseispteirgelgsvnqflicigialaialagplaaaplwrtnfgrvavipsvllaig 280
 QY 182 LLPLPAGT-----DETAKHDLIPLOGE-----APKLGGRPRYSFLDLFRA 224
 DB 281 mafspesprvlvqgkvseaeakltlygkervvelvrdlsasgqgssepegwfdlfs 340
 QY 225 RDNMRGRTTVGLVLFQOLTGPVNLVYASTIFSSVGHGSSAVLASVGLGAVKVAAT 284
 DB 341 r--ykwvsvgaalfiqqlaglnarvyystsvfrsagi---qsdvaasalgasnvfgt 395
 QY 285 LTAGMLVDRAGRALLAGCALMALSVSGILVSVFVPMDSGSPCLAVPNATGQTGLPGD 344
 DB 395 avasslmdkmgrksllitstfggmalsm-----lllsisftwkaaya 438
 QY 345 SGLQDSSLPPIPRTNEDQREPILSTAKTKPHRSGDPSAPPRLALSSALPGPPLPARG 404
 DB 423 -----lllsisftwkaaya 438
 QY 405 HALLRTALLCLMVFVSFAFSFGPGVPTWLVSEIYVPEIRAFACFNSFNNAANLFI 464
 DB 439 gtl-----avvgtyvlslfslgagvpalllpelfasrirakavalslgmhwnisnfvigl 494
 QY 465 SFULDIGTGLSWTFLLYGLTAVLGLGYLYLFVPEPKGOSLAIED 509
 DB 495 yflsvvktfgiasvylgfvagvcvavlvlyagnvvetkgrsleee 539

RESULT 12
 AAB12594
 ID AAB12594 standard; Protein; 491 AA.
 AC AAB12594;
 XX 09-NOV-2000 (first entry)
 DT Brevibacterium lactofermentum sugar transporter protein SEQ ID NO:6.
 DE Brevibacterium lactofermentum; glcBD; sugar transporter; breeding;
 KW corynebacterium; phosphoenolpyruvate-sugar transport system; PTS;
 KW non-PTS.
 XX Brevibacterium lactofermentum.
 OS
 PN WO200037497-A1.
 XX 29-JUN-2000.
 PD 16-DEC-1999; 99WO-JP07078.
 PF 18-DEC-1998; 98JP-0360620.
 PR (AJTN) AJINOMOTO CO INC.
 PA Kanno S, Kimura E, Matsui K, Nakamatsu T;
 PI WPI; 2000-442642/38.
 XX DR N-PSDB; AAA65400.
 OS

PT Sugar transporter gene gltBD of Brevibacterium lactofermentum, useful
 PT for production of coryneform bacteria with altered membrane sugar
 PT transport -
 XX Claim 1; Page 21-23; 26pp; Japanese.
 XX The present invention describes a protein which has a transmembrane sugar
 CC transport activity. The protein is specifically a non
 CC phosphoenolpyruvate-sugar transport system (PTS) sugar transporter.
 CC It can be used for in breeding corynebacteria with altered transmembrane
 CC sugar transport. The present represents the Brevibacterium lactofermentum
 CC sugar transporter encoded by the gltBD gene, which is used in the
 CC exemplification of the present invention.
 XX Sequence 491 AA;
 SQ

Query Match 18.2%; Score 504; DB 21; Length 491;
 Best Local Similarity 26.5%; Pred. No. 2.4e-37;
 Matches 139; Conservative 87; Mismatches 190; Indels 108; Gaps 9;

QY 12 ASVSLGLGLTFGYELAVISGALLPLQLDFGLSCLEEFVLVGSLLGALLASLVGGFLIDC 71
 DB 33 alvatfgglfgydgtvngalnptmreigltaftegvvtssllfgeaagamifgrisdh 92
 QY 72 YGRKQAILGSNLVLLAGSLTGLAGSLAMVLVGRVAVGFAISLSSMACCIYVSELVGPQR 131
 DB 93 wgrkrkiislaavafvgtmvcvfapfvamvgrvllglavgastvvpvylaelapfel 152
 QY 132 RGVLSLYEAGITVIGLLSYALNYALAGTIPW-----WRHMFQWATAPAVLQSLSLFLP 186
 DB 153 rgsilagrnelmivvgqlaafvln-alignvfhghdgwvrymlaiaaipaialffgmrlvp 211
 QY 187 AG-----TDET-ATHKDLIPLOGE-----PKLGGRPRYSFLDLFRARD 226
 DB 212 esprwlvergridearavletirpierahevadvhlarעהhavseksmgilreilsskw 271
 QY 227 NMRGRTTVGLVLFQOLTGPVNLVYASTIFSSVGHGSSAVLASVGLGAVKVAATLT 286
 DB 272 lvr-illvgiglgvaqqltginsimyyqvvlleaaf-senaalnanpagvliavvgaafi 329
 QY 287 AMGLVDRAGRALLAGCALMALSVSGILVSVFVPMDSGSPCLAVPNATGOTGLPGDSG 346
 DB 330 alwmmdrinrrtllitgyslttishvligiaslafp-----366
 QY 347 LIQDSSLPIPTNEDQREPILSTAKTKPHRSGDPSAPPRLALSSALPGPPLPARGHA 406
 DB 367 -----gdlrp-----372
 QY 407 LLRTWALLCLMVFVSFAFSFGPGVPTWLVSEIYVPEIRAFACFNSFNNAANLFI 466
 DB 373 ---yvlltvlvfvsgmqfllnavatwvmlseifplamrgfaigvsvffliwianafglff 429
 QY 467 LDLIGHTGLSWTFLLYGLTAVLGLGYLYLFVPEPKGOSLAIEDQ 510
 DB 430 ptmeavglgtgffmfgagvgvvaliflytqvpetgrtleeide 473

RESULT 13
 AAG89949
 ID AAG89949 standard; Protein; 491 AA.
 AC AAG89949;
 XX 26-SEP-2001 (first entry)
 DT C glutamicum protein fragment SEQ ID NO: 3703.
 DE Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX Corynebacterium glutamicum.
 OS

Query Match		18.1%; Score 500.5; DB 20; Length 518;
Best Local Similarity		27.6%; Pred. No. 5.4e-37;
Matches 161; Conservative 81; Mismatches 196; Indels 145; Gaps 14;		
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QY	49	-----FLVGSLLGALLASLVGGFLIDCYGRKQAILGSNLVLLAGSLTLGLAGSLAWL 101
Db	77	ydsqtlmtfsslylaallsslvastvtrfrgkxsmllgglifxgalingfaxhvwxl 136
QY	102	VLGRVVGFSAISLSSMACCIYVSEVLPORGVLSYELAGITVIGLLSVLALYALAGTP 161
Db	137	ivgrilfglrfandsvplixisemapykyrgalnigqfslsitvgilvanlvnyffakik 196
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QY	216	--YSFIDLFRARDN-----MRCRTTVGLGLVLPQQLTGOPNVLCYASTIF 258
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Db	311	sslgfk--ddaaamsavitgvnvvatecvsiygvdkwrralflegvqml-----360
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Db	382	-----lpkwaivvvlficiyysafawsgpl 408
QY	431	TWLVLSIYVETIRGAPAFCHSFNWAANLFISSLFDLI--GTIGLSWTFLYGLTAVL 488
Db	409	gwlvpseifplelraraqinsvnmflfllaqvfiltlchmkfgl----flrfatfvli 465
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KW	XX	termination sequence.
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